

On page 28, please amend the paragraph starting on line 14 to read:

A2
FIG. 1 shows yeast two-hybrid cloning, characterization, and expression of ILK. The full length ILK cDNA, Plac5, was isolated from a human placental library using the BIT-9 insert. Plac5 contains a 1509 bp open reading frame, with a presumptive initiator Met at nt 157, and an AAUAAA (SEQ ID NO: 13) signal 11 bp upstream of the polyadenylation site. *In vitro* transcription and translation of Plac5 in rabbit reticulocyte lysates yielded a protein of apparent Mr of 59 kDa. (b) A search of the PIR protein database indicated homology with protein kinase subdomains I to XI, as identified by Hanks et al. We note sequence variations in the ILK subdomains I, VIb, and VII, relative to catalytic domains of known protein kinases. Subdomain I (residues 199-213), does not have the typical GXGXXG (SEQ ID NO: 14) motif, although this region in ILK is Gly-rich. In subdomain VIb, Asp328 of ILK may compensate for the lack of the otherwise conserved Asp319. In subdomain VII, the DFG triplet is absent in ILK. The integrin binding site maps to amino acid residues 293-451 (BIT-9). The ILK kinase domain is most highly related to the CTR1 kinase of *Arabidopsis thaliana* (30% identity, P<10). The CTR1, B-raf, Yes and Csk kinase domains are aligned with Plac5. (c) Amino acid residues 33-164 comprise four contiguous ankyrin repeats, as defined by Lux et. al. (d) BIT-9 was used to probe a blot of poly A+ selected RNA (MTN I, Clontech) from various human tissues. (e) Whole cell lysates of mouse, rat and human cell lines (10 µg/lane) were analyzed by Western blotting with the affinity-purified 92-2 antibody (see description of methods in Example 3). The ILK sequence data are available from GenBank under accession number U40282.

In the figures:

On pages 1/23 to 6/23, please replace Figures 1a, 1b and 1c with the clean copies provided for Figures 1a, 1b and 1c.

REMARKS

Formal Matters

The present application has been amended to insert sequences with SEQ ID NOS. 13-21 in the Sequence Listing, and to insert the corresponding SEQ ID NOS. in the specification.